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                                     Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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Listing first 45 summaries
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                                                                                                 Kirihara, J.A., Petri, J.B. and Messing, J. Isolation and sequence of a gene encodin zein protein from maize Gene 71, 359-370 (1988)
                                                                                                                                                                                                                                                          MZEZEIN1OK 2562 bp DNA line Zea mays 10-kDa zein gene, complete cds. M23537 GI:340933 methionine-rich protein; seed storage protein; Zea mays 3-week old seedling leaf DNA.
                                                                                                                                                                                         Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoldeae; Andropogoneae; Zea.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 (bases 1 to 570)
Kirihara,J.A., Hunsperger,J.P., Mahoney,W.C. and Messing,J.W.
Differential expression of a gene for a methionine-rich storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Viridiplantae; Streptophyta; Er
Spermatophyta; Magnoliophyta; Liliopsida;
Clade; Panicoideae; Andropogoneae; Zea.
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Maize mRNA for 10kDa zein.
X07535
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Data kindly reviewed (20 June 1988) by MESSING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mol. Gen. Genet. 211 (3), 477-484 (1988)
88216260
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Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           storage protein;
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                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              protein in maize
                                                                                                                                140
                                          9.6%;
(larity 98.9%;
Conservative
                                                                                                                                D)
                                                                                                                                                            /note="
                                                                                                                                /note="polyA site"
151 c 127 g
                                                                                                                                                                                       MSQMMMPQCHCDAVSQINLQOQLPENENPMAMTIPPMFLQQPFVGAAF* 540. 545
                                                                                                                                                                                                                                /db_xref="maizeDB:Variation/58063"
/db_xref="SPTREMBL:Q41881"
/translation="makkwLalfallalCaSaTSaTHIPGHLPPVMPLGTMNPCMQYC
                                                                                                                                                                                                                                                                         /codon_start=1
/protein_id="CAA30409.1"
/db_xref="GI:22541"
                                                                                                                                                                                                                                                                                                                                   /tissue_type="endosperm"
/clone_lib="pUC119"
22, .474
                                                                                                                                                                                                                                                                                                                                                                            /strain="W23"
/db_xref="taxon:4577"
/clone="10kZ-1"
                                                                                                                                                                                                                     MMQQGLASLMACPSLMLQQLLALPLQTMPVMMPQMMTPNMMSPLMMPSMMSPMVLPSM
                                                                                                                                                                                                                                                                                                                   /note="10kDa zein (AA 1 -
                                                                                                                                                                                                                                                                                                                                                                                                                        /organism-"Zea mays"
                                                                                                                                                                                                                                                                                                                                                                                                                                                    ocation/Qualifiers
                                                                                                                                                                       "polyA signal"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           zein
                                           0
                                          Score 93.4; DB 8;
Pred. No. 1.7e-07;
0; Mismatches 1;
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ZM27KZNB/c
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AX027357/c
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Best Local s
Matches 126
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TITLE
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                                                                                                                                                                                                                                                                                                            AACATGT 12546
                                                                                                                                                                                                                                                                                                                                                                 CTATTAGTTTTTAAAAACGAATTTTAATTTGGGACAAAGAGTATATGAGAATTACAAG 12553
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Sequence
AX027357
                                                                                                                                                                                             Z.mays 27kDa zein
X56118
X56118.1 GI:22100
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Novel mads-box genes and uses thereof
Patent: WO 0037488-A 5 29-JUN-2000;
MAX PLANCK GESELLSCHAFT (DE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoldeae; Andropogoneae; Zea.
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                                     Sequence variation between alleles reveals two correction at the 27-kDa zein locus of maize Genomics 11 (4), 849-856 (1991)
                                                                                1 (bases 1 to 369)
Das, O.P., Ward, K.,
                                                                                                          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Trach
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaccae;
clade; Panicoideae; Andropogoneae; Zea
                                                                                                                                                      Zea mays
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Messing, J
                           92147128
                                                                                                                                                                    Zea mays.
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Similarity 67.4%;
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            (bases 1 to 3695)
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/db_xref="taxon:4577"
2725 c 2718 g
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                                                                                               to 3695)
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Patent W00037488.
                                                                                Ray, S. and Messing, J.
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Pred. No. 4.8e-07;
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aceae; PACC
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JOURNAL
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Best Local Similarity
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              mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Direct Submission
Submitted (24-SEP-1990) J. Messing, RUTGERS STATE UNIVERSITY,
WAKSMAN INSTITUTE, HOES LANE, PISCATAWAY NEW JERSEY 08855, U
Location/Qualifiers
                                                                                                                                                                                                           Submitted (13-DEC-1999) Agronomy, Submitted (13-DEC-1999) Agronomy, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Direct Submission
                                                                                                                                                                                                                                                           Hsia, A.P., Chen, W. and Schnable, P.S.
                                                                                                                                                                                                                                                                             Unpublished
2 (bases 1
                                                                                                                                                                                                                                                                                                        Alternative Transcription Start Sites and Polyadenylation Recruited during Mu Suppression at the rf2 locus of Maize
                                                                                                                                                                                                                                                                                                                                      1 (bases 1 to 17380)
Cui, X., Hsia, A.P., Wise, R.P. and Schnable, P.S.
                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Viridiplantae: Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
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                                                                                                                                                                                                Hall, Ames, IA 5001
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /tissue_type="Leaf"
2195. .2205
/note-"similar to sequence 3' to Zea mays cl coding region and sequence 5' to GapC4 coding region 2010, 3172, 3369. 5515,6042. .6184,6272. .6425,6533. .6762,13928. .14017,14115. .14288,14381. .14518,
                                                           /note="similar to 3' LTR of Zea mays retrosposon Milt" 2065. .3096
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /standard_name="Cap Site"
877 c 734 g 969
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/strain="A188"
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                                                                                       /map="between umc153 and sus1" 10. .465
                                                                                                                       /db_xref="taxon;4577"
/chromosome="9"
                                                                                                                                                   /organism="Zea mays"
/cultivar="B73"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /db_xref="taxon:4577"
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79.8%;
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factor 2 (rf2) gene,
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                    atgctaaaacgactaatattatgggacggagggagtactttatta 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                acaataaatctagacatatatataaaacacatacattaagtattgtatgaatctattaaa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   | tactccctaagtccccaatatattttagaccttaaattgtatgtctatattccaaaagaatg 195
                                                                                                                                                                                                                                                                                                                                                                                                                            AGGCTAAAATGGATTTTAATTTGGAACATAGGGAGTATATTCTAA 13755
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATAATGAATCTAGAC--ACATACAAAACACATACACTAATTATTGTATGAATCCAATAAA 13710
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       123;
                                                                                                                                                                                  AF466203

AF466203

AF466203

Zea mays clone ZMBBC_0092E12 putative RIRE2 orf3, putative gypsy-type retrotransposon RIRE2, putative porf1, regulatory protein, putative pol protein, putative gag protein, putative pol protein, putative gag protein, putative pol protein, putative gag protein, putative pol protein, putative gag-pol precursor orf1, putative gag-pol precursor orf1, putative protein, putative gag-pol precursor orf2, and putative prpol genes,
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Zea.

1 (bases 1 to 147198)
                                                                            Zea mays
                                                                                                   Zea
                                                                                                                                           AF466203.1
                                                                                                                                                                AF466203
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                                                                                                   mays
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/gene="rf2"
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4729 c 3855 g 4748 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GAALASHMDVDKIAFTGSTDTGKIILELAAKSNLKTVTLELGGKSPFIIMDDADVDHA
VELAHFALFFNQGQCCCAGSRTFVHERVYDEFVEKAKARALKRVVGDPFRKGVEQGPQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GVLQRFSTAAAVEEPITPSVHVNYTKLLINGNFVDSASGKTFPTLDPRTGEVIAHVAE,
GDAEDINRAVAAARKAFDEGPWPKWTAYERSRILLRFADLIEKHNDELAALETWDNGK,
PYEQAAQIEVPMVARLWRYYAGWADKIHGLIVPADGPHHVQILHEPIGVAGQIIPWNF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PHYTII and hml
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IDDEQFNKILRYIRYGVDGGATLVTGGDRLGDKGFYIQPTIFSDVQDGMKIAQEEIFG
PVQSILKFKDLNEVIKRANASQYGLAAGVFTNSLDTANTLTRALRAGTVWVNCFDVFD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PLIMYAWKYGPALACGNTLVLKTAEQTPLSALYISKLLHEAGLPEGVVNVVSGFGPTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="similar to regions
PHYTII and hml genes"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAIPFGGYKMSGIGREKGVDSLKNYLQVKAVVTPIKNAAWL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /product="T cytoplasm male sterility restorer factor 2"
/proteln_id="AAG49988.1"
/db_xref="G1:12004294"
/translation="MARRAASSLYSRCLLARAPAGAPPAAPSAPRRTVPADGMHRLLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /gene="rf2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="corresponding mRNA sequence deposited in
Accession Number U43082"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /codon_start=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="aldehyde dehydrogenase"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /gene="rf2"
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5533. .6762,13928. .14017,14115. .14288,14381.
14863. .15000,15119. .15180,15304. .15577)
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                                                                                                                                           GI:18568234
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Pred. No.
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                                                                                                                                                                                                                                                                                                                           PLN 07-FEB-2002
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.14518,
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TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AUTHORS
TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Llaca, V., Linton, E.W., Young, S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (07-JAN-2002) Department of Biological Sciences, University, West Lafayette, IN 47907, USA (bases 1 to 147198)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ramakrishna, W., S. Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Jersey, The Plant Genome Initiative at Rutgers
/translation="MGSLQQPLQPGTVLRPGSLEFMSLDGSYGMILLPPPRDSDNGGR
RPARRRNRRHLPRMYEEQHSSSPLPLPRQRRRRRGNQGQAGGRASSAVERIDIPSAP
TGGV9GVDLAFETKASAVPPRHANPEQMDDASALAEGLQDVALVPKTTTQSVPDVTMS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /rpt_unit=cya
/evidence=not_experimental
^ommlement(<9301_ .>12549)
                                                                                                                                                                                                                                                                                                                                                                         /product="putative gypsy-type retrotransposon
complement(<9301. .>12549)
/gene="2092E12.2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VEAESRAETIAADI.AAAQVAASEORARAGELESALDESAKALAEALAGAAEOREADLA
AMSEAVSDVYILIGSGDV95GSSPOSKLOALGDVARGKIREALHHGVRRAFAVLASHY
VVDLERVSEGYCLPDEDEAALAEVQRLDAVAAGPSAALATTTEAEILPAFSLEAEVD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RSGKRSHGQTDLAPRKALKTASVCAASAAPGVVVQPTLSQGVSPQGARASPVSGEQVP
EAGSSGALAI VIGEAGAAVVSSPLVVPAMLAPAATEVAAVVPGEERVAASVGMAVAS
APSASEEVGVVRSQVPGOSLIAVRRSPEARRQLLAFRTTREASDPVFILDDQEDOSW
DELRERAEATVGSLRSSLEVFCRDVPKILQDL/DRSAAKSSFIRCEVDVWGSLRSLRT
SLDGATARLSQQDAKVADLQLLCADLAAEAAAACAEAQRQRSEFYQVVEERDQSRGRA
                                                                                       /evidence=not_experimental
/product="putative gypsy-type
/protein_id="AAL75973.1"
/db_xref="GI:18568236"
                                                                                                                                                                                                                                                             complement(9301.
                                                                                                                                                                                                                                                                                                                         GB:AP002881.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                    /gene-"2092E12.2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6215.
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PSSQPPSGETPSVPGVGASGSWPEARGRPERSPDEAGGAFVAPEGGVBASAPGGFPL
VPAAHGGDPQVIATVPEPSAPRASKARVAPKLPVKRSSAAVSGAGIQETSPQARWIMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /product="putative RIRE2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     join(5148. .5420,5843. ...)
7419. .7764,7846. .8336)
/gene="z092E12.1"
/codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              join(<5148. .5420,5843. .
7419. .7764,7846. .>8336)
/gene="Z092E12.1"
                                                                                                                                                                                                                                 /gene="Z092E12.2"
                                                                                                                                                                                                                                                                                     /evidence=not_experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LTDGGDGTEGAAPSQGGA*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AFSQLRMRPDQGCVTLEVGWHKPSLPRVPEDAADGAARRVAAKEKKKKKDAEKARARE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /translation="MGGVAPSPPPGYVVSFVSFHERGEGVPTGRFMRAIMFHYGVELH
NLTPNSISQAAIFVAVCEGYLGIAPHWDLWTHLFFAELFALPTGERKVSAAMGKPDSH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GI:17082476"
                                                                                                                                                                                                         /codon_start=1
                                                                                                                                                                                                                                                                                                                                                    /note="similar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /evidence=not_experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="similar to Zea mays RIRE2 orf3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /gene="Z092E12.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 <5148.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /product-"putative RIRE2 orf3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone="ZMMBBc_0092E12"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /chromosome="2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /db_xref="taxon:4577"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /cultivar="B73"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Zea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ocation/Qualifiers
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                                                                                                                                                                                                                                                                                                                      to gypsy-type retrotransposon RIRE2 GI:11967907 (Oryza sativa)"
                                                                                                                                                                                                                                                             .12549)
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                                                                                                                                                                                                                                                                                                                   (Oryza sativa)"
                                                                                                                                             retrotransposon RIRE2"
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GGGGDDGDGSGRGGSKDGGGGSRGGSRGGSKGGSKRASC"
join(<22595. 22737,23370. 23524,23609. 23705,25250. 255
26050. 26427,26561. >26632)
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/product="regulatory protein"
<22595. >26632
                                                                                                                                                                                                                                                                                                                                                              complement(24021. .24051)
/note="AT-rich"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /translation="malsacpaqeellqpagrplrkqlaaaarsinwsyslewsisst
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RPVGSLSPEDLGDTEWYYYICMTYAFLDGQGLDGRSSASNEHVWLCNAHLAGSKUEPR
                                                                                                                                                                                                                                                                                                                                                                                                                                                              NEMFLYLKSLYPSIHKYDKASILAETIAYLKELQRRYQELESRRQGGSGCYSKKYCYG
SNSKRKSPEFAGGAKEHPWYLPMDGTSNYTYTYSDRDYLLEVQCLMEKLLMTRYFDAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ALLAKVPEDPDLINRATAAFREPQCPIYSEQPSSNPSADETGEAADIAVFEGLDHNAM
DMETAGIAVEGLDHNAMDMETVTAAAGRHGTGQELGEADSPSNASLEHITKGIDEFY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /evidence=not_experimental
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/db_xref="GI:18568238"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="Z.mays B-Peru
GB:X57276.1 GI:22194
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complement(19130. .19588)
/gene="Z092E12.3"
/codon_start=1
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complement(<19130. .>19588)
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/gene="z092E12.3"
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VLGRPCYAKFMDVPNYTYLKLKMPGPNGVITVGPTYKHAFECDVECVEYAEALAESEA
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SDKPITFNQADHPDHVPSPGKYPLVVDPIVGDVRLTKVLMDGGSCLNIIYTETLRLLR
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VAAAEYKNPRKPPGGANLFDKMLKESCPYHQGPVKHTLEECVMLRRHFHKARPPAEGG
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QPGESLRDYIRRFSKQRTELPNITDSDVIGAFLAGTTCRDLVSKLGRKTPTRASELMD
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WEASVYTGRTRNTAPAAPGHLGNEHHRRDRFAHLDERVRRGYHPRRGGRYDSGEDRSP
                                                                                                   GB:U68408.1 GI:1657766"
                                                                                                                           /gene="2092E12.6"
/note="similar to maize retrotransposon
                                                                                                                                                                                                  /product="putative pol protein"
<30970. .>32083
                                                                                                                                                                                                                                                                                           /evidence=not_experimental
join(<30970. .31268,31897. .>32083)
                                                                                                                                                                                                                                                                                                                                                                                                                              KSLHLDALSVQASALDGFMRLKIGAQFAGSGAVVPGMISQSLRKAIGKR"
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join(22595. .22737,23270. .2
26050. .26427,26561. .26632)
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/product="putative orfl"
/protein_id="AAL75974.1"
/db_xref="GI:18568237"
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/genem 2092E12.3"
/notem similar to Z.diploperennis Grandel gene GB:X82087.1
G1:609287"
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DEGAGALESIRRDVGQVWAGQPPAREIRHLPQGFQHRVANDVRVRPPPASSGVGQNLA
/gene="Z092E12.6"
                                                                   /evidence-not_experimental
                                                                                                                                                                                                                                                                  /gene="Z092E12.6"
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/codon_start=1
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GI:22194"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CAGCATAAAGCTGCAAAGGCCT 14246
Draft entry and computer-readable copy of sequence in [1] kindly provided by A.Boronat, 04-AUG-194087. There are three potential polyadenylation signals located at positions 1338 to 1343, 1392 to 1397 and 1405 to 1410.
                                                                                                                           Boronat,A., Martinez,M.C., Reina,M., Puigdomenech,P. and Palau,J. Isolation and sequencing of a 28 kd glutelin-2 gene from maize: Common elements in the 5' flanking regions among zein and gluteli
                                                                                                                                                                                                                                                                                                                                      glutelin
                                                                                                                                                                                                                                                                                                                                                                                                  Maize endosperm glutelin-2 gene,
                                                                                                                genes
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complement(<51801. .>54270)
/gene-"2092E12.9"
/note-"similar to maize retrotransposon Opie-2 gag gene
GB:U68408.1 GI:1657766"
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RSNGITPLTRFWYT"
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TSNVFLVESLGYNLLFDKSETQGTLKRFLRRAQNEFELKYKKIRSDNGSKFKNLQVEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /product="putative pol protein"
/protein_id="AAL75977.1"
/db_xref="GI:18568240"
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join(<44689. .44868,45357. .45548,46078.
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/protein_id="AAL75976.1"
/db_xref="GI:18568239"
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join(44689. .44868,45357.
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3B:U68408.1 GI:1657766"
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                                                                                                                                                                                                                                                                        Submitted (23-UN-1990) Reina M., Dept. of Biologia Molecular, C.I.D., C.S.I.C. Jordi Girona Salgado 18-26, 08034 Barcelona, Spain 2 (bases 1 to 2975)
Reina,M., Ponte,I., Guillen,P., Boronat,A. and Palau,J. 3 Sequence analysis of a genomic clone encoding a 2c2 protein from the paragraph of the paragraph of the protein from the paragraph of the p
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1 (bases 1 to 2975)
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                       /organism="Zea mays"
/strain="W64A"
/db_xref="taxon:4577"
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/db_xref="G1:168485"
/translation="MRVLLVALALLALAASATSTHTSGGGGGQPPPPVHLPPPVHLPP
/clone="p268c"
                                                                                                                                                     Location/Qualifiers
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/db_xref="taxon:4577"
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Zea mays 22 kDa alpha zein gene cluster, complete sequence.
AF090447 AF105716
AF090447.2 GI:13606087
                                                                                                                                                                                   Submitted (04-SEP-1998) Waksman Institute, Rutgers Frelinghuysen Road, Piscataway, NJ 08854-8020, USA 3 (bases 1 to 65155)
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Song,R., Llaca,V., Linton,E. and Messing,J.
Genomic Imprinting as a Rescue for a Compac
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Song, R.,
                                 Frelinghuysen Road, Piscataway, 4 (bases 1 to 346296)
                                                                                              Direct Submission
Submitted (10-NOV-1998) Waksman
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                                                                                                                                                           Llaca, V., Lou, A., Young, S. and Messing, J.
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   Llaca, V. and Messing, J.
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/db_xref="swiss-pROT:P04706"
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/translation="mrvtupalAtlaAsATSTHTSGGCGCOPPPPVHLPPPVHLPP
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698 c 595 g
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2519. .2524
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/db_xref="GI:22517"
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/note="zein zc2"
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2506. .2511
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/clone_lib="lambda Charon-35"
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79.8%;
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Pred. No. 0.0017
0; Mismatches
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                                                                Institute, Rutgers
NJ 08854-8020, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 8;
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                                                                                                                                                                                                                                                          University, 190
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EEVEGVQHDMAPQREVLLGRDMIGRSTSRTCSVGTWSVAPPRGLARYITEPLLEMLSF

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REFERENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (24-APR-2001) Waksman Institute, Rutgers Univer: Frelinghuysen Road, Piscataway, NJ 08854-8020, USA Amino acid sequence updated by submitter On Apr 12, 2001 this sequence version replaced gi:4416300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Frelinghuysen Road, Piscataway, NJ 08854-8020, USA Sequence update by submitter (bases 1 to 346296)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gi:4140643
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                                                                                                       VNEGSKANNAMSGGCGSGCGGGCGALF NASTAAGEGLHNKSAGCGGGGCGSGCGGGGG
CGSGMAIEGFKANHAKSGGCGSGCGGGCGTLFSSSAAAGQGOSRSGGCGSGCGGGCGS
CSMAAEGSNGGHAKSGGCGGGCGGGGGGGGGGGGGGGGATTTLSLMPGADVVTAEQESGTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /product="hypothetical protein"
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/protein_id="AAD20309_1"
/db_xref="61:4416304"
/translation="MVKLIGKVLEHDDTDADRSEGKKLDVGFTETTEQFESTFGVRYW
KAGSSATVPSSAQKVFTMVRMEPFSLKSCLLPHSIKDQNTGSWTRFVNDCGTELIRLQ
                   /evidence=not_experimental
/product="hypothetical protein"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         join(<3179. .4286,5020. .5155,5266. .5443,5892. .>602
/product="hypothetical protein"
join(3179. .4286,5020. .5155,5266. .5443,5892. .6020)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Zea mays"
/db_xref="taxon:4577"
/chromosome="4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /map="4s"
/Clone="cosmid III.3C12; V.9D7"
/note="inbred line BSS53"
join(<1256. .1397,2128. .>2300)
                                                                                                                                                                                                                                           {	t RCEELVGPAPTPTAFTIFYGGRKASLQRFACGACDGGDGELSFPLMKPYEIMEYLHN}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /map-"4s"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /db_xref="taxon:4577"
/chromosome="4"
/translation="MDVGWRPMTATRVDVERESRAHGDGLTGMSGVATGEAETTHGGG
                                                                                            /codon_start=
                                                                                                                                                                                                                                                                                                                                                                                                                                                         /codon_start=]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="inbred line BSS53"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone="BAC 204"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /product="hypothetical protein"
join(1256. .1397,2128. .2300)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone="cosmid II.2E10"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /db_xref="taxon:4577"
/chromosome="4"
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/note="target sequence duplication"
complement(50243. .50571)
/note="slmilar to grande 1"
complement(50572. .60252)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="target sequence duplication"
complement(39152. .49223)
/rpt_family="gypsy/Ty3-type retrotransposon"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /rpt_
24303
                                                                       /rpt_type=dispersed complement(50572 ...
                                                                                                                                                                                                                                                                                                  /pseudo complement(45973. .49223)
                                                                                                                                                                                                                                                                                                                                                                                                              complement(39152. .42406) complement(42452. .45283)
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GMEDPKVKTVLKNQEAISLMKSIKDPQAAAK"
15142. . 17012
                           /note="target sequence duplication"
complement(50577. .52000)
                                                                                                                                                                                                                                                                                    complement(49224. .49228)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /rpt_type=dispersed
complement(39147. .39151)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   complement(38797.
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HVECRSRAAQERAEQLAISQLFALVLLAFLYALGCYAVAAARYGRPPELPAVRHRRAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /rpt_type=dispersed 36025. .37602
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /translation="MSYQATVSSYGGNTAVMAKSFVMVVRSVAQTWYSSLRPGTITSW
QKLKDMLLISFQGFQTKPVTAQALFQCTQDHBBYLQAYVRRFLRLRAQAPTVPNEIVI
EAMIKGLRPGFSAQYFARKPPQTLEKLLQKMBBYIRADNDFRQRREEAFRFSEMTRGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AVELECROGDDAGAMEECAI"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PAPGPARLLELYVVAGGALADMCVEVLYSTHLRIFAGGEVNPAHLNDLEHGGMLLMFF
LFGALALASQLWPRHFPLTDGALCLVAATAFTAELVLFYFHSTTHMGLEGYYHYLLVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /product-"hypothetical protein"
/protein_id="AAD20312.1"
/db_xref="G1:4416307"
/translation="MGSFKGHVLPGTLFLAVGLWRVWSSAARHAAEPSSFRVRAWSPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          31759
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PEYYGNHPAVSVASASQPQASWHQPPPPPPLQQGQQPEGGQYAQHQRDFREQSEARTV
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/protein_id="AAD20308.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    24306
/note="copia-type retroelement PREM-2"
                                                                                                                         /note="nested in grande 1 retroelement"
/rpt_family="copia-type retroelement PREM-2"
                                                                                                                                                                                                                                                                                                                                                            /note="gypsy-type polyprotein"
/codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /rpt_type=dispersed
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /product-"hypothetical protein"
join(36233. .36579,37382. .3792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="php(PIO)20725 RFLP marker"
join(<36233. .36579,37382. >3792
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25532. .26569
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3. .24307
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Waksman Institute,

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SOURCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GCAAAATTGTCGGGGACCATAATTAGGGGTACCCTCAAGACGCCTAATTCTCAGCTGGTA 301417
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          84:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AR46646 DAA Illear PLN 07-FEB-20. Zea mays clone ZMMBBb_Z195D10 putative transposase gene, partial cds; glycyl-trNA synthetase, ornithine carbamoyltransferase, putative gag protein, putative SET-domain transcriptional regulator, putative oxysterol-binding protein, putative polyprotein, putative oxysterol-binding protein, putative gag-pol protein, putative gag-pol polyprotein, putative phosphatidylinositol-4-phosphate-5-kinase, hypothetical protein, putative gag-pol polyprotein, putative recotransposon protein, and proof genes, complete cds; and putative teosinte branched2; TB2 gene, partial
Submitted (07-JAN-2002) Genetics Department, University Wisconsin, Madison, WI 53706, USA 3 (bases 1 to 141939)
                                                                                                                                          Submitted (07-7AN-2002) Department of Biological Sciences, Purdue University, West Lafayette, IN 47907, USA 2 (bases 1 to 141939)
                                                                                                                                                                                                                          1 (bases 1 to 141939)
Ramakrishna, W., Emberton, J., SanMiguel, P. and Bennetzen, J
Direct Submission
                                                                                                                                                                                                                                                                                                       Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae; PACC Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae; PACC Spermatophyta; Andropogoneae; Zea.
                                                                                      Direct Submission
                                                                                                              Doebley, J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AF466646
AF466646.1
                                                                                                                                                                                                                                                                                                                                                                                                      Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                  Zea mays.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STGLVEVSCDVVFDETNGSQVEQVDLDEIGEEQAPCIALRNMSIGDVCPKESEEPPST
GDQPSSSMQASPTONEDEAQNOEGQNOEDGEPQDDSNDGGGDTNOEGKEDEEEPRP
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VEGLDPGETYAPVARLESIRILLAYATYHGFKLYQHDVKSAFLNGFIKEBVYVEDPPG
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TKYTODILTRFGMKDAKFIKTPHGTNHEHDLDTGGKSVDQKYYBBHGSLLYLCASRP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ISNVFLYDSLDYNLLSVSQLCQMGYNCLFTDIGVTVFRRSDDSIAFKGVLEGQLYLVD FDRAELDTCLIAKTNMGWLWHRRLAHVGMKNLHKLLKGEHILGLTNVHFEKDRICSAC QAGKQVGTHHPHKNIMTTDRPLELLHMDLFGPIAYISIGGSKVCLVIVDDYSRFTWVF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DIMLSVCMCARFQSDPKESHLTAVKRILRYLAYTPKFGLMYPRGSTFDLIGYSDADWA
GCKINRKSTSGTCQFLGRSLVSWASKKQNSVALSTAEAEYIAAGHCCAQLLWMRQTLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SYELLTGKKPNISYFRVFGSKCFILIKRGRKSKFAPKTVEGFLLGYDSNTRAYRVFNK
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PYTPQQNGVVERKNRTLLDMARTMLDEYKTPDRFWAEAVNTACYAINRLYLHRILKKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /product="copia-type pol polyprotein" complement(52949. .56140)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  complement(<56208.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /product="copia-type pol polyprotein"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DQLADIFTKPLDEQSFTRLRHELNILDSRNFFC"
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
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Submitted (08-JAN-2002) Rutgers, The State University of Jersey, The Plant Genome Initiative at Rutgers - Waksman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Llaca, V., Linton, E.W., Young, S., Kovchok, S. and Messing, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       190 Frelinghuysen Road, Piscataway, NJ 08854, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                          join(<7456. .7779,8407.
10092. .10260,10670. .110
/gene="z195D10.3"</pre>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note-"Similar to Arabidopsis thaliana glycyl-tRNA synthetase gene GB:AJ002062.1 GI:2564214 (Arabidopsis thaliana)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ÖYGLTNKVFAFTLDNASSNAAAMRLLRPÏMSPYLGIDNGVESEMFLHORGACHIINLI VKDALDALKILEFFETALSFLASKORIAATMKSYCLATK RPEKEGLDMEVRANSTY LALKHLEFHIKHALY PRAEGDOFILTDEHWVGEKVLKFLELFYGTVALLSG VY PETSLAKHLEFHIKHALY PRAEGDOFILTDEHWVGEKVLKFLELFYGTVALLSG VY PETSLAKHLFHIK VIAHLHALY SAROTHIRGVIQPALDK NKYMRNIPLLY SFAFILD PAKKKG FSRYLRHANTISTDY AVY QVTTRAKLTDVYNK Y EEKYGSVELNRVVPPNL SGKKRSAMDEI TUDDADWGTSVGMHSFRASTLNIARDTSATALLHAASSSASTASELIS SLLDGTVAOLTEDENILHWHQHKLTYPVLSIMAKDILI PVSTYSESTFSLTGRII
                                                                                                                                          carbamoyltransferase (OCTase): nuclear gene for chloroplast product GB:AF033562.1 GI:6578123"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /product="glycyl-tRNA synthetase"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /product="glycyl-tRNA synthetase"
<3895. .>6224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /evidence=not_experimental join(<3895. .3964,4131. .4403,5874. /gene="2195D10.2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                complement(2064. .2132)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /product="putative transposase" <80. .>1575
                                                       /evidence=not_experimental
join(7456. .7779,8407. .8520,8781. .8912,9006. .9281,
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                                                                                                                                                                                                                                                            /product="ornithine carbamoyltransferase"
<7456. .>12056
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DERRRIKSDVVEMLTCIKDWEDAEARMOHMVDDKELEETFEDLYLD"
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                              /gene="2195D10.3"
                                                                                                                                                                                                 /note="Similar to Canavalia lineata ornithine
                                                                                                                                                                                                                             /gene="Z195D10.3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /evidence=not_experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /gene="Z195D10.2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /evidence-not_experimental
join(3895_.3964,4131..4403,5874..5978,6073..6224)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="putative transposase"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /gene-"Z195D10.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /evidence=not_experimental
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partial 5') GB:AP002525.1 GI:8570079 (Oryza sativa)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /gene="2195D10.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone="ZMMBBb_Z195D10"
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/chromosome="5"
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/cultivar="B73"
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.5978,6073. .>6224)

.>12056)

gene

mRNA

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repeat_region
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                          LTEDRKKMLTPTTRIMVELALKRKLQNEKMANLVSLILPPIELDLKEIAÕTFSKFACN
AHTICDPELEPLGTGLYPVISIINHSCVPNAVLIFDGRTAVVRALDPINKDEEVSISY
IETATVTKKRNNDLKQYFFTGTGPPCVKGFDEDALLEGFRGKROACDGFILLPNSDKAE
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EPYASTPNKILVGSSCDHCFTSCNLRKCSNCRVTWYCSSNCQKEEWKLHQLECRAMAA
                                                                                                                                                                                                                                                                                                                                                                                                                  complement(join(34788. .34959,35820. .35886,36189] .3625
36676. .36782,37180. .37258,37356. .37454,37591. .37672,
37676. .37874,38851. .38925,39374. .39508,39656. .39801,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="similar to Arabidopsis thaliana hypothetical protein T13L16.8 gene (At2g17900) GB:AC003952.2 GI:6598398 (Arabidopsis thaliana)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                complement(join(<34788. .34959,35820. .35886,36189. .36258, 36676. .36782.37180. .37258,37356. .37454,37591. .37672, 37786. .37874,38851. .38925,39374. .39508,39656. .39801;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STONDDRGSQQQRPQCSSQASGQQQSSFRPPAPRGRGARGFRGREGDQPRRIFCLFCG
ENKCHTTRWCHVTTQKQKETAEAAAQQAQPKQVMHTASYHSPYIREYVGNHPALSVAS
ASQPQASWQQPPPPPPLQQGQQPEGSQYAPHQRDFREQSEARTVNSTVPESKHIY*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /product-"putative gag protein"
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\mathtt{WRLKIPFPRPRTVREAYGTGLLEFTEDALKSLTRAADILKVTHGVKSQF\mathtt{MKELFGKLE}
                                                                                                                                                                                                                                                                                                                                       /gene="Z195D10
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                                                                                                                                                                                                                                                                                                                                                                                                     40039.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /evidence=not_experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product="putative SET-domain transcriptional regulator"
complement(<34788. .>40150)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               40039. .>40150))
/gene="Z195D10.7
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complement(32540 ...32642)
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QTKPVTAQALFQCTQDHEEYLQAYVRRFLRLRAQAPTVPNETVIEAMIKGLRPGPSAQ
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complement(22204 . .23721)
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/gene="Z195D10.5"
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KFGGFTVGVWKGVVGVGCVWLVDRGCLVYPVGADAYFIKSEMFGGLYAKSERLSHLKT
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FRDLARLCADGGYOLRIRSLEGTPNYGPROTDIIILAVFFSVFLDILDLAKYAYVPVI
NGLTDYNHPCQIMADALTMLEQIGRIENTKVYYYVGDGNNIVHSWLLLADVLPFHFYCA
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/protein_id="AAL75995.1"
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                                                                                                                                              2-1-2, Tsukuba, Ibaraki 305-8602, Japan (E-mail:tsasaki@nias.affrc.go.jp, URL:http://rgp.dna.affrc.go.jp/, Tel:81-298-38-7441, Fax:81-298-38-7468)
NOTE: It currently consists of 1 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submitter. This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.

* NOTE: This is a 'working draft' sequence.

* This sequence will be replaced to be preserved.
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PROGRESS ***,
                                                                                                                                                                                                                                                                                                                                                                                                                                     Agrobiological Sciences, 2-1-2, Tsukuba, Ibaraki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (23-JAN-2002) Takuji Sasaki, National Institute of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sasaki, T., Matsumoto, T. and Yamamoto, K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Direct Submission
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/cultivar="Nipponbare"
                          /organism="Oryza sativa'
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/protein id="AAL75998.1"
/db_xref="GI:18568266"
/translation-"MHPFCCAPLVPVSPAASAAPAASSAVAGTQAVMPPPOPPDLPPP
PPRNNSATGGERRARAAGVSGGGGGDSSPLEGVKLNETVGGGISGINYKWVNYGRGWR
PRWFALHEGVLSTYKIHGPDRIILSRETERGAKVIGEESLARLNRPSAFSPSHSNGHH
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                                                                                                                                                                                                                                                Agrobiological Sciences, Rice Genome Research Program; Kannondai 2-1-2, Tsukuba, Ibaraki 305-8602, Japan
(E-mail:tasaski@nias.affrc.go.jp, URL:http://rgp.dna.affrc.go.jp/,
Tel:81-298-38-7441, Fax:81-298-38-7468)
NOTE: It currently consists of 1 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submitter. This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.

* This sequence will be replaced
by the finished sequence as soon as it is available and
the accession number will be preserved.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota: Viridiplantae: Streptophyta: Embryophyta; Tracheophyta;
Spermatophyta: Magnoliophyta: Liliopsida; Poales; Poaceae:
Ehrhartoideae: Oryzeae: Oryzea.
1 (bases 1 to 148138)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AP004395 148138 bp DNA Oryza sativa chromosome 7 clone P0030H06,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Direct Submission Submitted (05-DEC-2001) Takuji Sasaki, National Institute of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Oryza sativa (cultivar:Nipponbare) DNA, clone:P0030H06
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/chromosome="7"
/clone="P0475E07"
, 28755 c 29155 g 41331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               , Matsumoto, T. and Yamamoto, K.
                                                                                                        /clone="P0030H06"
30183 c 29741 (
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/chromosome="7"
                                                                                                                                                                                                  /organism="Oryza sativa"
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                                                                                                                                                                                 /cultivar="Nipponbare
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SanMiguel, P.J., Tikhon
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                                                                          /product-"alcohol dehydrogenase 1"
/protein_id="AAF43977.1"
/protein_id="AAF43977.1"
/db_xref="Gi:7262819"
/translation="MATAGKVIKCKAAVAWEAGKPLSIEEVEVAPPOAMEVRVKILFT
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$$CLHTDYNFWEAKGGTPVFPRIFGHEAGGIIESVGEVTVHFVGTSTFSEYTVMHVGCV
AHCKSAESNGDLLRINTDGGVAIADGKSRFSINGKBIYHFVGTSTFSEYTVMHVGCV
AKINPOAPLDKVLYVLSGGISTGLGASINVAKPPKGSTVAVFGLGAVGLAAAEGARIAG
AKINPOAPLDKVLYVLSGGISTGLGASINVAKPPKGSTVAVFGLGAVGLAAAEGARIAG
             ASRIIGVDLNPSREEEARKFGCTEFVNPKDHNKPVQEVLAEMTNGGVDRSVECTGNIN
AMIQAFECVHDGWGVAVLVGVPHKDAEFKTHPMNFLNERTLKGTFFGNYKPRTDLPNV
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
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AX099698.1 GI:13538752
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1 (bases 1 to 879)
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1 (bases I to 879)

Anderson, H.M., Chay.C.A., Chen.G. and Conner, T.W.

Plant regulatory sequences for control of gene expression

Patent: WO 0119976-A 54 22-MAR-2001;
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                                   ron-glycogen-like polysaccharides in a host. The method comprises transforming a host, suitable for fermentation, with genes encoding starch- or glycogen-synthesis enzymes, and fermenting the transformants. The specification also describes hosts transformed with a gene active in glycogen synthesis and at least one non-starch branching gene, involved in production of amylopectin or amylose in its original host. The method is used to produce plant-like starches by fermentation and new starches in plants. These starches are useful for all food and non-food applications of starch. The present sequence is used in the course of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Producing non-glycogen-like polysaccharides in bacteria, fungi
plants - transformed with genes for enzymes involved in starch
glycogen synthesis allows fermentative production of starches
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Query Match Best Local S Matches 126

Local Similarity

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Score 89.4; D Pred. No. 2.1e 0; Mismatches

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RESULT 3
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kernels, for conferring or improving disease resistance, generating late or early flowering, expressing heterologous proteins in the upper florets in the spikelets of grass inflorescence, modifying solute partition in florets, improving kernel derived products or the expression of enzymes affecting any agronomic aspect of the kernel or the whole inflorescence. Compounds identified as being activators or inhibitors of genes specifically expressed in the spikelets of grass inflorescence may be used as growth regulators and/or herbicides.
                                                                                                                                                                        gene which encodes a MIKC-type MADS-box protein. The protein is involved in DNA-binding and is expressed in the upper florets of spikelets of grass inflorescences. The ZMM8 and ZMM14 genes (see AAA5132-23) map to chromosomes 1 and 9, respectively, and are similar to OSMADS1 from rice (Oryza sativa). The ZMM8 and ZMM14 genes are useful for study of MADS-box proteins in monocotyledons. The sequences can be used to produce transgenic plants having altered level or composition of protein(s) in the florets of spikelets, for modulating the number of
                                                                                                                                                                                                                                                                                                                                                                                                     Novel nucleic acids encoding proteins with the activity of proteins expressed in the upper florets of spikelets of grass inflorescences useful for producing plants with altered proteins levels or
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                                                                                                                                                                                                                                                                                                  This is a regulatory region sequence from the maize (Zea mays) ZMM14 gene which encodes a MIKC-type MADS-box protein. The protein is invo
                                                                                                                                                                                                                                                                                                                                                       Disclosure; Page 88-91;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (PLAC ) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN
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Mascarenhas
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T Isolated pollen-specific promoter from W-22 corn - used to T express genes to inhibit pollen prodn., induce toxicity in pests or enhance nutritional value

WPI; 1992-064456/08

Claim 8; Fig 2 (a-d); 12pp; English.

A cDNA library made to poly(A) RNA isolated from mature pollen of maize was constructed. One of the cDNA clones from the library, Zml3, was selected for detailed characterization. Zml3 represents a gene that is present in a very few copies in the corn geneome. It is 929 nucleotides in length and in addition has a 47 nucleotide poly(A) tail. Primer extension analysis indicates that Zml3 is a full length copy of the mRNA, which codes for a predicted polypeptide that is 170 AA residues long and has a mol. wt. of 18.3 kb. The hydropathy profile strongly suggests a signal peptide at the amino terminus. The function of this protein is not yet known. A genomic clone corresp. to Zml3 was isolated by screening a genomic library of the inbred maize line W-22. The cDNA clone is colinear with the genomic clone with no introns being present.

Sequence 2710 BP; 720 A; 711 C; 620 G; 659 T; 0 other;

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RESULT
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XX AAF8
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                                                                                                                                                                                                                                                                                                                                                                                                           The present invention relates to novel corn promoter sequences (see AAF81456-AAF81478). The promoter sequences are useful for conferling expression of a second polynucleotide molecule in a transgenic plant tissue. In addition, the promoter sequences are useful for providing plants with herbicide resistance. The promoter sequences are suitable selectively modulating expression of any operatively linked gene and provide additional regulatory element diversity in a plant expression vector in gene stacking approaches. The present sequence is one such contents of the present sequence is one such contents.
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                                                                                                                                                                                                                                                                                                                                       Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         transgenic plant; herbicide resistance;
                                                                                                                                                                                                                                                                                                                                          264 A; 192 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              entry)
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92.38;
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                                                                                                                                                                                                                                                                                                                                                                                             in the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ВP
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Pred. No. 2
                                                                                                                                                                                                           Score 68.8; DB 22;
Pred. No. 2.6e-05;
0; Mismatches 72;
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                                                                                                                                                                                                                                                                                                                                          136 G;
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                                                                                                                                                                                                                                                                                                                                             287 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 15,
2.3e-05;
6;
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ARESULT AAFB1457
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention relates to novel corn promoter sequences (see AAF81456-AAF81478). The promoter sequences are useful for conferring expression of a second polynucleotide molecule in a transgenic plant tissue. In addition, the promoter sequences are useful for providing plants with herbicide resistance. The promoter sequences are suitable selectively modulating expression of any operatively linked gene and provide additional regulatory element diversity in a plant expression vector in gene stacking approaches. The present sequence is one such operator sequence isolated in the present invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Corn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             08-JUN-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel promoter nucleic acid sequences useful for regulating heterologous gene expression in plants, comprising regulatory sequences located upstream to plant DNA structural coding sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200119976-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 879
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; Pages 90-91; 101pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22-MAR-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 transgenic plant; herbicide resistance;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              264 A; 192 C; 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           #700164347
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                                                                                                                                                                                                                                                                                                                                                          Score
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                                                                                                                                                                                                                                                                                                                                                          .6e-05;
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                                                                                                                                                                                                                                                                                                                               72;
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RESULT 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A maintainer gene of plants, pref. a foreign chimeric gene, comprises (a) a ferility restorer gene which comprises a fertility restorer DNA and (ii) a restorer promoter capable of directing the expression of the fertility restorer DNA and (b) a gollen lethality gene that is selectively expressed in microspores and/or pollen of the plant to prevent the production of functional pollen and which comprises (i) a pollen lethality DNA and (ii) a gollen specific promoter capable of directing expression of the pollen specific promoter ransformed with this DNA (maintainer C plants) can be used to maintain a homogenous population of male promoter is a pollen specific promoter and is used in the construction of a plant transformation vector comprising a maintainer and as Americal
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Best Local S
Matches 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Maintainer gene for maintenance of male-sterile plants - comprises fertility-restorer gene and pollen-lethality gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 2661 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Maintainer gene; sterile; sterility; seed; fertility restorer gene; pollen
                                                                                                                                                                      maintainer gene as described.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 1; Page 47-49; 87pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Leemans J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (PLBZ ) PLANT GENETIC SYSTEMS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12-JUN-1992;
03-NOV-1992;
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92US-0970840
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96.4%;
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n lethality
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gene; Zea mays; ds.
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RESULT 10 ABL34027/c

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Best Local Similarity

Matches 110; Conserv
                                                                                                                       2375
                                                                                                                                                                                                                                                                                  The present invention provides the protein and coding sequences of maize zinc finger transcription factor Ramosa I (Ral). The protein is involved in the regulation of the plant meristem identity and architecture. The sequences can be used to produce transgenic plants with a reduced number of branches which would produce higher-yielding primitive plants, and allow them to be planted at high density, and to produce other plants with an increased number of branches which would give greater fruit, seed and pollen yields per plant. The present sequence is a mutated version of the coding sequence of the invention.
2261 CAATAATTCACTAAAACAAATTTTAATTTGGAACAGAGAGTATAAGATATAAGT 2208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Zea mays.
Synthetic.
                                                                                                                                                                                                                                                        Sequence 4936 BP; 1304 A; 1176 C; 1051 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 16; Fig 11; 90pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New maize Ramosa 1 protein which exhibits zinc finger protein transcription factor capable of influencing meristem identity and branch development in plants, useful for improving yield and health
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Martienssen RA, Vollbrecht E;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22-MAY-2001; 2001WO-US16659
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        misc_signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (COLD-) COLD SPRING HARBOR LAB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22-MAY-2000; 2000US-206136P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  pollen; zinc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Maize;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Maize Ramosa 1 coding sequence with insertion mutations
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAS19028 standard; DNA; 4936 BP
                               249
                                                                                                                                  129 tatcotttactccctaagtcccaatatttttagaccttaaattgtatgtctatattcaa 188
                tattaaaatgotaaaacgactaatattatgggacggagggagtactttattagt 302
                                                         ATAAATGATGATAAATCTAGACACATATACAAAAT----ATCAAGAATTGTTTGAATC
                                                                       TACTCGCTCCGTCTTAAAATAATATTCGTTTTAACTATTGTTTTTATCTATATATTCAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2002-097651/13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ral; Ramosa 1; meristem identity; branch number; fruit yield;
; zinc finger transcription factor; transgenic plant; mutant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAU11823
                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers 2906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /standard_name= "transcriptional start site"
                                                                                                                                                                                             6.1%;
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                                                                                                                                                                             Score 59.2; DB 2
Pred. No. 0.0033;
0; Mismatches 5
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ABL34027

ABL34027 standard; DNA; 17594

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Best Local S
                                                                                                                            14676
                                                                                                                                                                              14736
                            14556
                                                                                                                                                                                                                                                                                                                                                               The present invention provides a number of human immune system associated genes which are modified by the methylation of cytosines. The sequences can be used in the diagnosis and treatment of immune system disorders, including eye diseases such as retinopathy, neovascular glaucoma and
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nucleic acid comprising fraction diagnosis and treatment cytosine methylation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          antirheumatic; antiarthritic; antidiabetic; antipsoriatic;
antiinflammatory; cancer; eye disease; arteriosclerosis; anaemia;
acute_myeloid_leukaemia; Alzheimer's disease; AIDS; epilepsy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; immune system disease; cytosine methylation; antiasth antiarteriosclerotic; antianaemic; cytostatic; nootropic; neuroprotective; anti-HIV; anticonvulsant; ophthalmological;
                                                                                                                                                                                                                                                                                                                            macular degeneration, arteriosclerosis, anaemia, cancer, acute my leukaemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel
                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; SEQ ID NO 2000; 32pp + Sequence Listing; German
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Olek
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30-JUN-2000;
01-SEP-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           03-JAN-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         26-MAR-2002
                                                                                                                                                                                                                                                                                          Sequence 17594
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  neurofibromatosis; rheumatoid arthritis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (EPIG-)
                                                                                                                                                    187
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                                                                                                totattaanatgotaanacgactaatattatgggacggagggagtactttattagtagat 306
                                                                                                                                                annagantgacantanatotagacatatatataanacacatacattaagtattgtatgan 246
tartaccargreeaattrrgaartatatatetaggreegeatccgreegeatcgr 423
                                                                                                                                                                              attatcctttactccctaagtcccaatatattttagaccttaaattgtatgtctatattc 186
                            261;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EPIGENOMICS
                                                                                                                                                                                                                                          Similarity
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                                                                                                                                                                                                                                                                                                                   The
                                                                                                                                                                                                                             Conservative
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2000DE-1043826
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                                                                                                                                                                                                                                                                                                                present sequence is a gene of the
                                                                                                                                                                                                                                                                                          BP; 5843 A;
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                                                                                                                                                                                                                                       5.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   fragment of chemically modified ment of diseases associated with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Berlin
                                                                                                                                                                                                                                                                                          96 C;
                                                                                                                                                                                                                               0;
                                                                                                                                                                                                                            Score 56; DB:
Pred. NO. 0.01:
0; Mismatches
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                                                                                                                                                                                                                                                                                            G; 8229 T; 0 other
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                                                                                                                                                                                                                                           .018;
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                                                                                                                                                                                                                                                    24;
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                                                                                                                                                                                                                               300;
                                                                                                                                                                                                                                                      Length 17594;
                                                                                                                                                                                                                                                                                                                    invention.
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abnormal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                useful
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Query Match Best Local

Similarity

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Score Pred.

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Sequence

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RESULT 11
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                                                             The present invention relates to novel corn promoter sequences (see AAF81456-AAF81478). The promoter sequences are useful for conferring expression of a second polynucleotide molecule in a transgenic plant tissue. In addition, the promoter sequences are useful for providing plants with herbicide resistance. The promoter sequences are suitable
                                                                                                                                                                                                                                                                                                                                                                                                   Corn promoter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAF81465
                                provide additional regulatory element diversity in a plant expression vector in gene stacking approaches. The present sequence is one such
                                                                                                                                Claim 1; Pages 93-94; 101pp; English.
                                                                                                                                                     Novel promoter nucleic acid sequences useful for regulating heterologous gene expression in plants, comprising regulatory located upstream to plant DNA structural coding sequences
                                                                                                                                                                                                                                                                                         13-SEP-2000; 2000WO-US25078.
                                                                                                                                                                                                                                                                                                                                     WO200119976-A2
                                                                                                                                                                                                                                                                                                                                                                               Corn;
                                                                                                                                                                                                                                                                                                                                                                                                                          08-JUN-2001
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                                                      selectively modulating expression of any operatively linked gene and
                                                                                                                                                                                                                        Anderson HM,
                                                                                                                                                                                                                                                                    16-SEP-1999;
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                                                                                                                                                                                                                                             (MONS ) MONSANTO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              promoter;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     standard; DNA;
                    sequence
                                                                                                                                                                                                                                                                                                                                                                                                                         (first
                                                                                                                                                                                                                                                                                                                                                                                                   clone #700333814.
                                                                                                                                                                                                                       Chay CA,
                                                                                                                                                                                                                                                                    9905-0154182
                                                                                                                                                                                                                                                                                                                                                                              transgenic plant;
                      isolated
                                                                                                                                                                                                                                                                                                                                                                                                                          entry)
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                      in the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                689
                                                                                                                                                                                                                        Conner
                      present
                                                                                                                                                                                                                                                                                                                                                                                herbicide
                                                                                                                                                                                                                                                                                                                                                                                resistance;
                                                                                                                                                                   sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14199
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RESULT 12
AAC86507/c
ID AAC86507/c
ID AAC86507/c
AC AAC865
XX AAC865
XX IS AAC865
XX IS AAC865
XX IS AAC865
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Matches
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                                                                                                                                                                                      modulating gene. The recombinant DNA molecules are useful for producing fertile, transgenic plants capable of regulated expression of a cytokinin modulating gene in developing seeds. They are also useful for improving stress tolerance and yield stability in plants. The preferential expression of recombinant DNA molecules of the invention occurs about 14-25 days after pollination. The transgenic plants thus produced have enhanced levels of cytokinin expression exhibit improved seed size, decreased tip kernel abortion and increased seed set during
                                                                                                                                                                                                                                                                                                                                                                                 invention. It comprises, in this order, a barley promoter, an Agrobacterium isopentenyl transferase (ipt) gene fragment, and a maize terminator. The DNA molecules of the invention comprise a genetic construct consisting of a promoter directing temporal and/or spatial gene expression in plant seed operatively linked to a cytokinin
                                                                                                                         Sequence
                                                                                                                                                                         unfavourable
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present sequence represents a recombinant DNA molecule
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  tolerance
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Habben JE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel recombinant DNA construct useful for producing transgenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16-APR-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA comprising
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                          Local Similarity
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       80;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             enhanced levels of cytokinin expression, improved stress
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Page 69-70; 76pp; English.
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     Conservative
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                                                                                                                                                                      environmental
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Score 54.2; DB
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D; Mismatches
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                                      cytokinin modulating gene in developing seeds. They are also useful for improving stress tolerance and yield stability in plants. The preferential expression of recombinant DNA molecules of the invention occurs about 14-25 days after pollination. The transgenic plants thus produced have enhanced levels of cytokinin expression exhibit improved seed size, decreased tip kernel abortion and increased seed set during
                                                                                                                                    genetic construct consisting of a promoter directing temporal and/or spatial gene expression in plant seed operatively linked to a cytokinin modulating gene. The recombinant DNA molecules are useful for producing fertile, transgenic plants capable of regulated expression of a
                                                                                                                                                                                                     invention. It comprises, in this order, a maize promoter, an asyrobacterium isopentenyl transferase (ipt) gene fragment, and a stuberosum terminator. The DNA molecules of the invention comprise
                               unfavourable environmental
                                                                                                                                                                                                                                                      The present sequence represents a recombinant DNA molecule
                                                                                                                                                                                                                                                                                        Disclosure;
                                                                                                                                                                                                                                                                                                                    Novel recombinant DNA construct useful for producing transgenic plants having enhanced levels of cytokinin expression, improved stress tolerance and yield stability -
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Solanum tuberosum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        temporal gene expression; spatial gene expression; plant seed; cytokinin modulating gene; transgenic plant; seed size; stress tolerance; yield stability; tip kernel abortion; seed set; isopentenyl transferase;
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Sequence

2722 BP; 732 A;

610 C;

619

G;

761 T; 0 other;

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31-JAN-2000;
04-FEB-2000;
24-FEB-2000;
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3471..3689

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2157..3393
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180..319
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320..2053
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102..179
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11-JUL-2000;
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18-APR-2000;
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                                   Isolated lipid metabolism polypeptide for screening to identify antagonists and agonists that may enhance or block activities m_\ell by lipid metabolism proteins and also for testing and detection
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2000US-0241809.
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Example

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453pp; English

The present invention describes a transformed cereal plant seeds endosperm having an elevated level of at least one preselected amino acid (aa) compared to a seed from a corresponding untransformed plant, where the aa is selected from lysine, cysteine, threonine, tryptophan, arginine, valine, leucine, isoleucine, histidine or their combinations, and optionally methionine. Plants transformed to express a heterologous

protein that has an elevated content of a

preselected amino

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RESULT 15
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                                                Example 2; Page 42-43;
                                                             5
                                                                   Plant seeds containing elevated
                                                                                                               (PION-) PIONEER HI-BRED
                                                                                                                                                                                                                   Chimeric gene construct gz::BHL::gz designated PHP11427
                                                                                                                                                                                                                                              AAZ08721;
                                                                                                                                                                                                                                                                                        Ranch
                                                                                                   Beach
                                                                                                                             09-FEB-1998;
                                                                                                                                          27-JAN-1999;
                                                                                                                                                      12-AUG-1999
                                                                                                                                                                   WO9940209-A1
                                                                                                                                                                                Hordeum vulgare.
                                                                                                                                                                                       Synthetic
                                                                                                                                                                                                   alteration;
                                                                                                                                                                                                       Hordeum vulgare; alpha
                                                                                                                                                                                                                                  20-OCT-1999
                                                                                                                                                                                                                                                           AAZ08721
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                                                             cereals
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                           standard;
                                                                                            Dress VM,
Rao AG;
                                                                                                                                                                                                   endosperm;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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                                                                                                                            98US-0020716
                                                                                                                                         99WO-US02061
                                                                                                                                                                                                                                                           DNA;
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                                               49pp;
                                                                                                   Ertl
                                                                                                                                                                                                  nutrition;
                                                                                                                                                                                                       hordothionin; HT12; modification;
                                                                                                               INT INC
                                                                                                                                                                                                                                                          5173
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                                                English.
                                                                                                                                                                                                                                                          ВР
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                                                                  preselected
                                                                                                  Higgins
                                                                                                                                                                                                 cereal; barley;
                                                                                                  RK,
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                                                                   amino
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                                                                                                 Jung
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                                                                   acid
                                                                                                  77
                                                                                                                                                                                                cation; plant seed; chimeric gene; ss.
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CC used to grow seeds, especially cereals, that have an endosperm with an CC increased content of the preselected maino acid, and therefore having an CC increased nutritional value. The transformed cereals can be used in feed CC formulations for animals. Transforming plants to have an elevated level CC of a preselected amino acid in the endosperm of its seed is advantageous CC in production of feed formulations. Feed formulations currently require CC essential nutrients, which are necessary for their growth. The methods contents such as allergenicity or anti-nutritional quality. The mutritional content of seeds without detrimental side currently require CC increase the nutritional content of seeds without detrimental side currently such as allergenicity or anti-nutritional quality. The nutritional content of the seeds is increased whilst maintaining a high CC quietd. The amount of preselected amino acid in the seed is increased at CC corresponding untransformed seed. The present sequence represents a CC chimeric gene construct produced in the construction of the HT12 gene construct produced in the construction of the HT12 gene which is derived from the barley (Hordeum vulgare) alpha hordothionin or the mature protein.
Search completed: September 9,
Job time: 9501 sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 5.6%;
Best Local Similarity 65.0%;
Matches 80; Conservative
                                                                                                                                                                                                                                                                                                            Sequence 5173 BP; 1527 A; 1154 C; 1170 G; 1322 T; 0 other;
                                                                                                                                                                           2653 TTT 2651
                                                                                                                                                                                                                                                   272
                                                                                                                                                                                                                                                   tat 274
                                      2002, 03:23:34
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Pred. No. 0.035;
0; Mismatches 43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 20; Length 5173;
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Title:
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Maximum Match 1008
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OM nucleic - nucleic search, using sw model
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     September 8, 2002, 23:09:28; Search time 1695.72 Seconds (without alignments) 7736.560 Million cell updates/sec
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Resul	NO.	Score	Query Match		DB	: #
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	6	86	8.8	536	12	вн217817
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	9	81.8	8.4	933	12	BH128804
	10	81.4	8.4	498	10	BF728645
	11	78.8	8.1	548	12	BH414177
	12	76.4	7.9	535	10	BM267973
	13	76.4	7.9	553	10	BM33281(
O	14	74	7.6	583	9	AI677352
	15	72.2	7.4	341	12	BH23070
	16	72	7.4	483	12	BH126949
O	17	72	7.4	805	2	10000

ALIGNMENTS

BASE COUNT	FEATURES Source	REFERENCE AUTHORS TITLE JOURNAL COMMENT	RESULT 1 AW120150/c LOCUS DEFINITION ACCESSION VERSION VERSION KEYWORDS SOURCE ORGANISM
/organism="R2a mays" /cultivar="W23" /db_xref="taxon:4577" /db_xref='taxon:4577" /clone_lib="614 - root cDNA library from Walbot Lab" /tissue_type="root" /dev_stage="3-4 days old" /lab_Nost="XLOLR" /note="07gan: root; Vector: pBlueScriptII SK+; Site_1:	Department of Biological Sciences Stanford University 855 California Ave, Palo Alto, CA 94304, USA Tel: 650 723 2227 Tex: 650 725 8221 Email: walbot@stanford.edu Plate: 614085 row: E column: 09. Location/Qualifiers 1496	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Zea. 1 (bases 1 to 496) Walbot, V. Maize ESTs from various cDNA libraries sequenced at Stanford University Unpublished (1999) Contact: Walbot V	AW120150 AW6 bp mrNA linear EST 22-OCT-1999 614085E09.y1 614 - root cDNA library from Walbot Lab Zea mays cDNA, mRNA sequence. AW120150 AW120150.1 GI:6095483 EST. Zea mays. Zea mays.

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BASE COUNT
ORIGIN
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Plate: 614085 row: E column:
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                                                                                                                                                                                                                                                                                                                                        Department of Biological Sciences
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/dev_stage="3-4 days old"
/lab_host="xlolR"
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855 California Ave, Palo Alto,
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished (1999)
Contact: Walbot V
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EcoRI; Site_2: XhoI; 3-4 days
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/cultivar="w23"
/db_xref="taxon:4577"
/clone_lib="614 - root cDNA library from
/tlssue_type="root"
/tlssue_type="root"
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACÇ

clade; Panicoideae; Andropogoneae; Zea.

1 (bases 1 to 509)
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Maize genomic sequences 
Unpublished (2001)
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Contact: Schroeder S
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Missouri Maize Project-Maize Mapping Project.
Parti Zea mays B73 PstI leaf tissue library
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209 Curtis Hall, Columbia, MO
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/tissue_type="Leaf"
/lab host="DH5 alpha"
/note="Organ: Leaf; Vector: PUC19; PstI digested B73
/genomic sucrose gradient size fractionated fragment sof 0.5kb to 2kb ligated to pUC19 transformed in DH5 cof 10.5kb to 2kb ligated to pUC19 transformed in DH5 cof 10.5kb to 2kb ligated to pUC19 transformed in DH5 cof 10.5kb to 2kb ligated to pUC19 transformed in DH5 cof 10.5kb to 2kb ligated to pUC19 transformed in DH5 cof 10.5kb to 2kb ligated to pUC19 transformed in DH5 cof 10.5kb to 2kb ligated to pUC19 transformed in DH5 cof 10.5kb to 2kb ligated to pUC19 transformed in DH5 cof 10.5kb to 2kb ligated to pUC19 transformed in DH5 cof 10.5kb to 2kb ligated to pUC19 transformed in DH5 cof 10.5kb to 2kb ligated to pUC19 transformed in DH5 cof 10.5kb to 2kb ligated to pUC19 transformed in DH5 cof 10.5kb to 2kb ligated to pUC19 transformed in DH5 cof 10.5kb to 2kb ligated to pUC19 transformed in DH5 cof 10.5kb to 2kb ligated to pUC19 transformed in DH5 cof 10.5kb to 2kb ligated to pUC19 transformed in DH5 cof 10.5kb to 2kb ligated to pUC19 transformed in DH5 cof 10.5kb to 2kb ligated to pUC19 transformed in DH5 cof 10.5kb to 2kb ligated to pUC19 transformed in DH5 cof 10.5kb to 2kb ligated to pUC19 transformed in DH5 cof 10.5kb to 2kb ligated to pUC19 transformed in DH5 cof 10.5kb to 2kb ligated to pUC19 transformed in DH5 cof 10.5kb to 2kb ligated to pUC19 transformed in DH5 cof 10.5kb to 2kb ligated to pUC19 transformed in DH5 cof 10.5kb to 2kb ligated to pUC19 transformed in DH5 cof 10.5kb to 2kb ligated to pUC19 transformed in DH5 cof 10.5kb to 2kb ligated to pUC19 transformed in DH5 cof 10.5kb to 2kb ligated to pUC19 transformed in DH5 cof 10.5kb to 2kb ligated to 2kb ligate
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Possible ligation site of ends cut by 2 different endonucleases.
Reverse complemented post-ligation sequence from source sequence.
Plate: 1006119 row: 44
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855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 725 8221
Fax: 650 725 8221
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/dev_stage="adult"
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/db_xref="taxon:4577"
/clone_lib="1006 - RescueMu Grid G"
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                  GI:16809845
                                                                     1006 - RescueMu
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57.1%;
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Pred. No. 7.2e-05;
                                                                                      536 bp
                                                                     Grid
                                                                   G Zea mays genomic,
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ATATTTCT 412
                                                                                AAGATATTTCGTATTTAATCTAATAATATTTTTTTGAGATCATACACATTGATATTTG
                                                                                                                                                           TTAATTTGAGACGGAGGGAGTAGTATTCATGTTTATGGC--TCCAAATTAATTTATTATA
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                                                                                                                                                                                                                                                                                                                       CAGTCATTTAAGCTCTAGATTTTTATGTATATATTCATATGGATGATTACGAAGATAAAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         855 California Ave, Palo Alto,
Tel: 650 723 2227
Fax: 650 725 8221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Class: transposon-tagged
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PMail: walbot@stanford.edu
Possible ligation site of ends cut by 2 different endonucleases.
Reverse complemented post-ligation sequence from source sequence.
Plate: 1006059 row: 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Maize genomic sequences found using engineered RescueMu transposon
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism-"Zea mays"
/cultivar-"mixed background W23/A188/B73"
/db_xref-"taxon:4577"
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AW231854
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BG320733
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                                                                                                                                                                                                                                                                                                                                         84;
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855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
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Spermatophyta; Magnoliophyta; Liliopsida;
Clade; Panicoldeae; Andropogoneae; Zea.
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/dev_stage="14, 21, 28, and 35 days after pollination"
/dev_stage="14, 21, 28, and 35 days after pollination"
/lab_host="E. coll SQLK"
/note="Organ: embryo; Vector: pBluescript SK; Site_1: XhoI
; Site_2: EcoRI; Library was prepared by Statagene using
the Uni-ZAP XR system (Stratagene BN937328-12). Clones
were picked by a Q-bot after blue/white selection
(ampicillin resistance - use 100 micrograms/microliter).
Developed from a pool of equal amounts of RNA from
developing embryos sampled at 14, 21, 28 and 35 days after
pollination of the Illinois High Oil Maize Strain Cycle
90: This closed strain has been selected for high Oil
concentration for 90 generations and originates from the
1890s era open pollinated variety Burr's White"
49 a 145 c 149 g 146 t
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/db_xref="taxon:4577"
/clone_lib="687 - Early embryo from Delaware"
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Pred. No. 0.00029;
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                                                                                                                                                                                                               Zea mays.
Zea mays
                                                            Meyers,B.C., Tingey,S.V. and Morgante,M. Abundance, distribution and transcriptional activity of elements in the malze genome Genome Res. 11 (10), 1660-1676 (2001)
                                                                                                                                                                                                                                                      GSS.
                                                                                                                                                                                                                                                                                                     G-3p3 Maize
clone G-3p3
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Dupont Genomics
                   Suite 200
                               Contact: Morgante
                                                    21475670
                                                                                                                                                                                                                                                                    BH128804
BH128804.1
                                                                                                                                                                                                                                                                                                                                            BH128804
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Singh, J.A., Wakui, K., Couroux, P., De Moors, A., Harris, L.J., J.I., Ouellet, T., Robert, L.S., Sprott, D. and Tinker, N.A. Expressed Sequence Tags from Cold-Stressed Maize Seedlings
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: singhja@em.agr.ca.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished (2001)
Contact: Singh, J.A
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140 c 130 g 205 t 19 others
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/cultivar="CO328"
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/tlssue_type="Leaf, crown"
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/clone="Zm04_06h05"
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Pred. No. 0.00026;
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Best Local :
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Local Similarity 73.8%;
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Zea mays
                                                                                             Tel:
                                                                                                                                         Contact: Walbot v
Department of Biological
                                                                                                                                                                                                                                                   Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoldeae; Andropogoneae; Zea.
                           Email: walbot@stanford.edu
Plate: 1000065 row: C colu
Location/Qualifiers
                                                                                                          855 California Ave, Palo Alto,
                                                                                                                           Stanford University
                                                                                                                                                                          Unpublished (1999)
                                                                                                                                                                                    Maize ESTs from various cDNA libraries sequenced at Stanford University
                                                                                                                                                                                                                         Walbot, V.
                                                                                                                                                                                                                                                                                                                                      EST
                                                                                                                                                                                                                                                                                                                                                      BF728645.1
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Sequences were trimmed to include only high quality bases; forward reverse reads were assembled when significant overlaps were
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PO Box 6104, Newa
Tel: 302 631 2638
Fax: 302 631 2607
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/dev_stage="seedling"
/note="Vector: pCR-Script; Total genomic
: ends were polished with Pfu polymerase
cloned into pCR-Script."
a 159 c 170 g 306 t
/organism="Zea mays"
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/sex="hermaphrodite"
/tissue_type="leaf"
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/clone="G-3p3"
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Pred. No. 0.00029;
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RESULT 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Maize genomic sequences found using engineered RescueMu transposon Unpublished (2001)
Contact: Walbot V
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Stanford University
855 California Ave, Palo Alto, CA 94304, USA
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                                                                                                                                                                                                                                                                                                                                                          Class: transposon-tagged
                                                                                                                                                                                                                                                                                                                                                                                           Possible ligation site of ends cut by 2 different endonucleases. Reverse complemented post-ligation sequence from source sequence Plate: 1007036 column: 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: walbot@stanford.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Walbot, V
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (bases 1 to 548)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                selected for the Unigene set. All singlets were also selected.
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/db_xref="taxon:4577"
/db_xref="taxon:4577"
/clone_lib="1000 - Unigene I from Maize Genome Project"
/clone_lib="1000 - Unigene I from Maize Genome Project"
/note="This library represents the unique ESTs found in
/note ESTs found in
/not
                                                                                        /cultivar="mixed background W23/A188/B73"
/db_xref="taxon:4577"
/clone_lib="1007 - RescueMu Grid H"
/tissue_type="leaf"
/dev_stage="adult"
                                                                                                                                                                                                                                                                                                           Location/Qualifiers
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Pred. No. 0.00041;
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BM267973
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Expressed Sequence Tags from B73 Maize: various stages and tissues including seedlings treated with a variety of hormones Unpublished (2001)
                                                                                                                                                                                                          rt). Overall sequence quality assessment and vector trimming were conducted using the Lucy software (<a href="http://www.tlgr.org/softlab/">http://www.tlgr.org/softlab/</a>). Lucy parameters were set to ensure an overall trimmed quality of 97.5% or better without any vector fragments in the chosen high-quality region of each sequence. Low-quality bases between the poly-T and the high-quality region were replaced with N's to serve
                                                                                                                                                                                                                                                                                                                                                                                                                                                    G405 Agronomy, Iov
Tel: 515-294-0975
Fax: 515-294-2299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Patrick S. Schnable Schnable Laboratory Iowa State University
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MEST375-A01.T3 ISUM5-RN Zea
                                                                  FORMARD: primer T7-1 (AA TAC GAC TCA CTA TAG)
BACKWARD: primer T3 (ATT AAC CCT CAC TAA AG)
Seq primer: primer T3 (ATT AAC CCT CAC TAA AG)
LOCALION/QUAlifiers
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                                                                                                                                                                                                                                                                                                                                                                               Phred software,
                                                                                                                                                                                                                                                                                                                                                                                                        Email: schnable@iastate.edu
Individual basecall and confidence value were assigned using the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  clade; Panicoideae; Andropogoneae; Zea.
                                                                                                                                                                      PCR PRimers
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/organism="Zea mays"
/cultivar="B73"
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97.68;
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Pred. No. 0.
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BM332810.1
EST.
                                                                                                                                                                        wen,T.J., Qiu,F., Guo,L., Ashlock,D.A and Schnable,P.S. Expressed Sequence Tags from B73 Maize: various stages and tissues including seedlings treated with a variety of hormones Unpublished (2001)
Contact: Patrick S. Schnable
Schnable Laboratory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae; PACC
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EMail: Schnable@iastate.edu
                                          Fax: 515-294-2299
                                                                                                                                                                                                                                                                                                                                                                                                                                                     clade; Panicoideae; Andropogoneae;
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                                                                   Agronomy, Iowa State University, Ames, IA 50011-1010, 515-294-0975
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/inote-"vector: pT7T3PAC; Site_1: ECORI; Site_2: NOTI;
/inotes-"vector: pT7T3PAC; Site_1: ECORI; Site_2: NOTI;
/inotes-"vector: pT7T3PAC; Site_1: Site_2: NOTI;
/inotes-"vector: pT7T3PAC; NOTI;
/inotes-"vector: pT7T3PAC;
/inotes-"vector: pT7T3P
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Pred. No. 0.0026;
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                                            AI677352 583 bp mRNA linear EST 02-FEB-2000 605053H02.x1 605 - Endosperm cDNA library from Schmidt lab Zea mays
cDNA, mRNA sequence AI677352
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BACKWARD: primer T3 (ATT AAC CCT CAC TAA AG)
Seq primer: primer T3 (ATT AAC CCT CAC TAA AG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 148
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tissues: Germinated seed and seedlings (1, 2, 8, 11 DAG),
Mixed mature tissures (17, 21, 38, 69, 77 DAG), Kernels
(3, 5, 10, 15, 20, 25, 30, DAP), Adventious roots (65 DAG),
Tassel (3-39 cm, 53 and 56 DAG), Immature ear (0.2-3, 0 cm, 53, 56, 59 DAG), Husk (73 DAG), Silk, unpollinated
first ear, ear shank, etiolated seedlings, callus,
Cycloheximide-treated callus, Anaerobic treated seedlings
(Cycloheximide-treated callus, Anaerobic treated seedlings,
NAA (a-Naphthalone acetic acid)-treated seedlings,
Kinetin-treated seedlings, ACG
(1-aminocyclopropane-1-carboxylix acid)-treated seedlings,
Brassinolide-treated seedlings, ABA (Abscisic acid)
-treated seedlings, GA (Gibberellic acid)-treated
seedlings, JA (Jasmonic acid)-treated seedlings, ds-cDNA
molecules were generated as follows. First-strand cDNA was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ds-cDMAs were digested with NotI and size-selected. The resulting molecules were directionally cloned into the EcoRI and NotI sites of the pT/T3PAC vector. The library then went through one round of normalization to COT value of 5 based on the methods of Marcelo Bento Soares (Genome Research 6: 791-806, 1995)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          resulting DNA:RNA hybrid was treated with RNase H and used as a template for DNA Poli-catalyzed second strand synthesis. After the addition of EcoRI adaptors, the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /tissue_type="mixed"
/lab_host="DH108"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="Vector: pT7T3PAC; Site_1: EcoRI; Site_2: NotI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone_lib="ISUM5 RN"
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/clone="MEST177-H02"
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Pred. No. 0.0026;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         74 TAGAAATATTTGTGTTGTATCGAATAATGAGTTGACATGCCATCGCGTGTGACTCATTAT 15
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                                                                                                                                                                                                                                                                                                                                        BH230702 341 bp DNA linear GSS 08-
1006159B04.x1 1006 - RescueMu Grid G Zea mays genomic, DNA
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Location/Qualifiers
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855 California Ave, Palo Alto, CA 94304,
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Spermatophyta; Magnoliophyta; Liliopsida;
clade; Panicoideae; Andropogoneae; Zea.
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                                                                Stanford University
                                                                                  Department of Biological Sciences
                                                                                                 Contact: Walbot V
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                                                                                                                                Walbot, V.

Maize genomic sequences found using
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                                               855 California Ave,
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650 725 8221
1: walbot@stanford.edu
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walbot@stanford.edu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="Organ: Kernel; Vector: pAD-GAL4-2'; Site_1: EcoRI;
Site_2: XhoI; Kernel endosperm cDNA library from Schmidt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /tissue_type="nucellar, embryo, and endosperm"
/dev_stage="10-14 days post-pollination"
/lab_host="DH5(alpha)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /db_xref="taxon:4577"
/clone_lib="605 - Endosperm cDNA library from Schmidt lab"
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/cultivar="Ohio43"
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; Poales; Po
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                                                                                               AGCATAAAGCTGCAAAGGCCT 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Possible ligation site so sequence was trimmed. Post-ligation sequence submitted separately. Plate: 1006159 row: 18
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                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   pBlueScript backbone); Site_1: BamHI; Site_2: BglII; RescueMu is a 4.9 kb, modified maize Mu transposon designed to allow plasmid rescue from total genomic DNA. Mu elements insert preferentially into transcription units. For more information on RescueMu, go to the web site 'www.zmdb.lastate.edu' and follow the links for 'RescueMu.' Grid G was grown at Stanford in 2000. DNA was extracted from leaf punches, double digested using BamHI and BglII, and ligated to form circular plasmids. DH10B and BglII, and ligated to form circular plasmids.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               cells were transformed and then screened on LB plates with ampicillin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               pBlueScript backbone); Site_1: BamHI; Site_2: BglII;
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/db_xref="taxon:4577"
/clone lih="""
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /tissue_type="leaf"
/dev_stage="adult"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone_lib="1006 - RescueMu Grid G"
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78.7%;
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                   9, 2002, 02:45:00
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             Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB seq length: 0
DB seq length: 2000000000
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42
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1: /cgn2_5/ptodata/2.

2: /cgn2_6/ptodata/2.

3: /cgn2_6/ptodata/2.

4: /cgn2_6/ptodata/2.

5: /cgn2_6/ptodata/2.

6: /cgn2_6/ptodata/2.
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                                                    GenCore version 4.5
Copyright (c) 1993 - 2000 Com
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/cgn2_6/ptodata/2/ina/6A_COMB.seq:*
/cgn2_6/ptodata/2/ina/6A_COMB.seq:*
/cgn2_6/ptodata/2/ina/6B_COMB.seq:*
/cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
/cgn2_6/ptodata/2/ina/backfiles1.seq:*
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        1 US-08-351-413-1

US-08-998-416-595

4 US-08-998-416-595

4 US-08-796-101-12

US-08-487-8268-13

2 US-08-487-8268-13

2 US-08-66-398-9

US-08-566-398-9

US-08-566-398-9

US-08-105-483-220

US-08-105-483-220

US-08-105-483-220

US-08-220-151-62

US-08-413-118-62

US-08-413-118-62

US-08-413-118-62

US-08-413-118-62

US-08-413-118-62

US-08-413-118-62

US-08-413-118-62

US-08-413-118-62

US-08-413-118-62

US-08-413-118-657-39

US-08-418-1009-68

US-08-417-210A-66

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40.2	40.2	40.2	40.2	40.2	40.6	41	41	41	41	41	41	41	41	41	41	4.1	41
4.1	4.1	4.1	4.1	4.1	4.2	4.2	4.2	4.2	4.2	4.2	4.2	4.2	4.2	4.2	4.2	4.2	4.2
2116	2096	2096	2096	2096	872	4427	4427	3750	3622	3622	3622	3460	3460	3460	3209	3209	3209
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US-07-811-048-9	PCT-US95-02945-1	US-08-278-630A-10	US-08-205-508-1	US-08-458-084-1	US-08-998-416-487	US-09-085-273-48	US-08-658-665-48	US-08-617-860B-19	US-09-085-273-60	US-08-796-101-24	US-08-658-665-60	US-09-085-273-57	US-08-796-101-21	US-08-658-665-57	PCT-US96-00547-27	US-09-354-138-39	US-09-085-273-27
Sequence 9, Appli	Sequence 1, Appli	Sequence 10, Appl	Sequence 1, Appli	Sequence 1, Appli	ς.		Sequence 48, Appl		Sequence 60, Appl	Sequence 24, Appl	Sequence 60, Appl	Sequence 57, Appl	Sequence 21, Appl	Sequence 57, Appl	Sequence 27, Appl	Sequence 39, Appl	Sequence 27, Appl

ALIGNMENTS

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Sequence 1, Application US/08351413
Patent No. 5750867
                                                                                                             TELEX: 248345
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2661 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: Williams, Mark
APPLICANT: Leemans, Jan
TITLE OF INVENTION: Maintenance of male-sterile plants
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
                                  HYPOTHETICAL: NO
                                                                                                                                                                                                                               NAME: Svenson, Leonard R.
REGISTRATION NUMBER: 30,330
REFERENCE/DOCKET NUMBER: 2121-102PCT
TELECOMMUNICATION INFORMATION:
TELEPAN: (703) 205-8000
TELEFAX: (703) 205-8050
                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0
FILING DATE: 03-NOV-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/899,072
FILING DATE: 12-JUN-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy
                   ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA:
                                                                         MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE: V
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: 8110 Gateho
CITY: Falls Church
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 800
ORGANISM: Zea mays
                                                                                                TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER:
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Y: U.S.A.
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                                                                                              linear
                                                          NO
                                                                         DNA (genomic)
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US-08-351-413-1
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Best Local Similarity
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                                                                                                                       INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         tent No.
                                                                                                                                                                  REGISTRATION NUMBER: 30,330
REFERENCE/DOCKET NUMBER: 2121-102PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 205-8000
                                                                                                                                                                                                                                                       APPLICATION NUMBER: US 07/899,072
FILING DATE: 12-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/970,849
FILING DATE: 03-NOV-1992
ATTORREY/AGENT INFORMATION:
                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 2661 base pairs
                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 800
PRIOR APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
FILING DATE:
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MEDIUM TYPE: Floppy disk
         TOPOLOGY: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Williams, Mark
APPLICANT: Leemans, Man
TITLE OF INVENTION: Mintenance of male-sterile plants
NUMBER OF SEQUENCES: 17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  950 tcagcataaagctgcaaaggcct 972
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    891 tgtcggggaccataattaggggtaccctcaatggctcctaattctcagctggtaaccc-ca 949
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: BIRCH, STEWART, KOLASCH & BIRCH STREET: 8110 Gatehouse Road, Suite 500 East CITY: Falls Church
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JOURNAL:
                                                                                                                                        TELEFAX: (703
TELEX: 248345
                                                                                                                                                                                                                           NAME: Svensson, Leonard R. REGISTRATION NUMBER: 30,3
                                               STRANDEDNESS:
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                                                              nucleic acid
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             DNA (genomic)
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Pred. No. 1.7e-07;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                               TELEFAX: 919-541-8689
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                  REFERENCE/DOCKET NUMBER: PF
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-541-8587
                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 31-DEC-1996
ATTORNEY/AGENT INFORMATION:
NAME: Meigs, J. Timothy
                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: CH 0016/97
                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Rebischung, Corinne
TITLE OF INVENTION: GENOMIC DNA SEQUENCES OF ASHBYA GOSSYPII
TITLE OF INVENTION: AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2385 TCAGCGTAAAGCTGCAAAGGCCT 2407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PUBLICATION INFORMATION:
AUTHORS: Hamilton et al.
 MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               950 tcagcataaagctgcaaaggcct 972
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VOLUME: 2
PAGES: 208-
DATE: 1989
                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/08/998,416 FILING DATE: 24-DEC-1997
                                STRANDEDNESS:
                                                                                                                                                                                     REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                       CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                      OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Zea mays
STRAIN: inbred line W-22
                  TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE:
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                                                                 LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ESSEE: No. 6239264artis Corporation ET: 3054 Cornwallis Road Research Triangle Park
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                                               nucleic acid
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                                                             658 base pairs
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Knechtle, Philipp
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Steiner, Sabine
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DNA (genomic)
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Pred. No. 1.7e-07;
0; Mismatches 2;
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US-08-796-101-12/c; Sequence 12, App.
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                                                                                                                                                                                                                                                                                                                               Patent No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                     GENERAL
                             CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
                                                                  SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                      TITLE OF INVENTION: RESTENOSIS/
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ORGANISM:
REGISTRATION NUMBER: TELECOMMUNICATION INFO
                                                                                                                                                                                                               NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                     APPLICANT:
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                                                                                                                                                                   STREET:
                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                    NAME:
                                                  APPLICATION NUMBER: FILING DATE: 05-FE
                                                                                                                                              COUNTRY:
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6183752
                 KOWALSKI, THOMAS J.
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Pred. No. 0.043;
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Matches
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TELEPAS: (212) 764-5574
INFORMATION FOR SEQ ID NO: 12
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: LIM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                              CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                 SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
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ATTORNEY/AGENT
                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES:
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TYPE: nucleic acid
STRANDEDNESS: single
                                               FILING DATE:
                                                                                                                FILING DATE:
                                                                                                                                                                                                                                                                                     STATE:
                                                                                                                                                                                                                                                                                                                    STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         97 GTAGT
                FILING DATE:
                              APPLICATION NUMBER:
                                                               APPLICATION NUMBER:
                                                                                                                                APPLICATION NUMBER:
                                                                                                                                                                                                                                                                   COUNTRY:
                                                                                                                                                                                                                                                                                                                                    ADDRESSEE:
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wes 141; Conserv
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1800 Diagonal Road,
                                                                                                                                                                                                                                                                   USA
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INFORMATION:
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RECOMBINANT FOWLPOX VIRUS
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                              EP 91
                                                               US/07/935,313
                                                                                                                               US/08/232,463
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NAME: BENT, Stephen A REGISTRATION NUMBER: :

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Best Local :
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pairs
                                                                                                                                                                                                    APPLICANT: Su, Xin-zhaun
APPLICANT: Wellems, Thomas E.
TITLE OF INVENTION: BINDING DOMAINS FROM PLASMODIUM VIVAX
TITLE OF INVENTION: AND PLASMODIUM FALCIPARUM ERVTHROCYTE BINDING PROTEINS
NUMBER OF SEQUENCES: 45
                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                         APPLICANT: Sim, Kim L.
APPLICANT: Chitnis, Chetan
APPLICANT: Miller, Louis H.
APPLICANT: Peterson, David
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REFERENCE/DOCKET NUMBER: 30.
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
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                                                                                                              ADDRESSEE: Knobbe Martens Olson & Bear STREET: 620 Newport Center Drive 16th CITY: Newport Beach STATE: California
            COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                 COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Match 4.3%; Score 42.2; D
Local Similarity 7.6%; Pred. No. 0.26;
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TELEFAX: (703)683-4109
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                                                                                                                                                                                                                                                                                       Peterson, David S.
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PatentIn Release #1.0, Version #1.25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local s
Matches 149
                                                                                                                                                                                                                                                                                                        Sequence 13, Application US/08487826B Patent No. 5993827
                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                        APPLICANT: Sim, Kim L.
APPLICANT: Chitnis, Chetan
APPLICANT: Miller, Louis H.
APPLICANT: Miller, Louis H.
APPLICANT: Peterson, David S.
APPLICANT: Su, Xin-zhaun
APPLICANT: Wellems, Thomas E.
APPLICANT: Wellems, Thomas E.
TITLE OF INVENTION: BINDING DOWAINS FROM PLASMODIUM VIVAX
TITLE OF INVENTION: AND PLASMODIUM FALCIPARUM ERYTHROCYTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HYPOTHETICAL: I
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REFERENCE/DOCKET NUMBER: NI
TELECOMMUNICATION INFORMATION:
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NAME: Israelsen, Ned
                                                                                                                                                                                                                                                                                                                                                                                                                   3795 TAAATTAATA 3804
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                                                                                                      CORRESPONDENCE ADDRESS
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                                                                                                                             NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                            307 tacattgtta 316
COUNTRY: US
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER:
FILING DATE: 10-SEP
                                  STATE:
                                                       CITY: Newport Beach
                                                                     STREET:
                                                                                      ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9 tttgtgttgtatcgaataatgagttgacatgccatcgcgtgtgactcattattaacaata 68
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                                                                   E: Knobbe Martens Olson & Bear 620 Newport Center Drive 16th Floor
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                                                                                                                                              BINDING
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COMPUTER READABLE FORM: MEDIUM TYPE: Floppy

Floppy disk

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RESULT 8
US-08-417-210A-116/c
; Sequence 116, Application US/08417210A
; Patent No. 5863542
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                                                                                                          GENERAL INFORMATION:
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                      APPLICANT: COX, WILLIAM I.
TITLE OF INVENTION: IMMUNODEFICIENCY RECOMBINANT POXVIRUS
NUMBER OF SEQUENCES: 148
                                                                                                                                                                                                                                                                                                                                               4385
                CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                            4445
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                                                                             APPLICANT:
                                                                                              APPLICANT:
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HYPOTHETICAL: NO
ANTI-SENSE: NO
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NAME: ISTACLSCO, Ned
REGISTRATION NUMBER: 29,655
REFERENCE/DOCKET NUMBER: NI
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                         205
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     ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: FILING DATE: 10-SEF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                             TARTAGLIA, JAMES
                                                                                           PAOLETTI, ENZO
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CURTIS, MORRIS & SAFFORD, P.C
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619) 235-0176
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Pred. No. 0.56;
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US-08-566-398-9/c
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; MOLECULE TYPE:
US-08-417-210A-116
                                                                                                                          Sequence 9, Application US/08566398
Patent No. 5888373
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches 140;
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                             APPLICANT: Paoletti, Enzo
APPLICANT: Gettig, Russell
TITLE OF INVENTION: RECOMBINANT POXVIRUS - FELINE IN
TITLE OF INVENTION: PERITONITIS VIRUS, COMPOSITIONS
TITLE OF INVENTION: MAKING AND USING THEM
NUMBER OF SEQUENCES: (CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION:
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Local Similarity 45.9%;
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release "'
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05-APR-1995
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Pred. No. 0.36;
0; Mismatches 1
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                                                    AND METHODS FOR
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ADDRESSEE:

E: Curtis, Morris & 530 Fifth Avenue

Safford, P.C

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                                                                                                                                                                 Patent No. 5858373
GENERAL INFORMATION:
                                                                                                                                                                                                     Sequence 51,
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/566,398 FILING DATE: 01-DEC-1995
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LENGTH: 2989 base pair
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                   APPLICANT: PROJECTI, Enzo
APPLICANT: Gettig, Russell
TITLE OF INVENTION: RECOMBINANT POXVIRUS - FELINE INFECTIOUS
TITLE OF INVENTION: PERITONITIS VIRUS, COMPOSITIONS THEREOF,
TITLE OF INVENTION: MAKING AND USING THEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 840-3333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: DNA (genomic)
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                                  CORRESPONDENCE ADDRESS:
                                                       NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           277
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STRANDEDNESS: single
TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                 97 GTAGT 93
                ADDRESSEE:
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E: Curtis, Morris & Safford, P.C 530 Fifth Avenue
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                                                                                                                                                Paoletti, Enzo
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Pred. No. 0
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                                                                                                      Patent No. 5494807
GENERAL INFORMATION:
GENERAL TRADICANT: Paoletti, Enzo
APPLICANT: Paoletti, Enzo
TITLE OF INVENTION: GENETIC
TITLE OF INVENTION: STRAIN
                                                                                                                                                                                Sequence 220, Application US/08105483 Patent No. 5494807
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/566,391
FILING DATE: 01-DEC-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION:
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ATTORNEY/AGENT INFORMATION:
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                                                                    CORRESPONDENCE ADDRESS:
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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STATE:
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REFERENCE/DOCKET NUMBER: 454310-2880
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH:
                              ADDRESSEE: Curtis, Morris & Safford ADDRESSEE: c/o William S. Frommer
                STREET:
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New York
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212) 840-0712
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Gaps

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85

COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk

ZIP: COUNTRY:

10036

NY

USA

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US-08-220-151-62/c
; Sequence 62, Application US/08220151
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Best Local Similarity
Matches 140; Conserv
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STRANDENESS: single
TOPOLOGY: linear
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 840-3333
NUMBER OF SEQUENCES: 91
CORRESPONDENCE ADDRESS:
ADDRESSEE: Curtis, Morris & Safford
STREET: 530 Fifth Avenue
                                                                        APPLICANT: Paoletti, Enzo
APPLICANT: Limbach, Keith J.
TITLE OF INVENTION: CANINE HERPESVIRUS 9B, 9C
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LENGTH: 3209 base pair
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APPLICATION NUMBER: US 0
FILING DATE: 06-MAR-1992
ATTORNEY/AGENT INFORMATION:
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                                                                             SEQUENCES OF AND G
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; Patent No. 5688920
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                                                                                                                                                                                                                                                          RESULT 13
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Best Local Similarity 45.9%;
Matches 140; Conservative
                                                                         GENERAL INFORMATION:
APPLICANT: PAOLETI, ENZO
APPLICANT: LIMBACH, KEITH J.
APPLICANT: LIMBACH, KEITH J.
TITLE OF INVENTION: NUCLECTIDE AND AMINO ACID SEQUENCES OF
TITLE OF INVENTION: CANINE HERPESVIRUS 9B, 9C, AND 9D AND USES THEREFOR
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TELEX: 425066 CURTMS
INFORMATION FOR SEQ ID NO:
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REFERENCE/DOCKET NUMBER: 454310-2540
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 840-3333
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LENGTH: 3209 base pair
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CURRENT APPLICATION DATA:
                                      CORRESPONDENCE ADDRESS:
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                                                                NUMBER OF SEQUENCES:
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OPERATING SYSTEM:
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SYSTEM: PC-DOS/MS-DOS
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CURTIS, MORRIS & SAFFORD, P.C. O FIFTH AVENUE, 25TH FLOOR
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                                                                                                                     Sequence 90, Application US/08224391 Patent No. 5744140
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Best Local Similarity
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TELEFAX: (212) 840-07
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08,
FILING DATE: 30-MAR-1994
ATTORNEY,ACENT INFORMATION:
NAME: FROMMER, WILLIAM S.
REGISTRATION NUMBER: 25,50
                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 3209 base pair
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPOTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
                                                 APPLICANT: Paoletti, Enzo
APPLICANT: Pincus, Steven E.
TITLE OF INVENTION: FLAVIVIE
                 CORRESPONDENCE ADDRESS
                                NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          324 TCTTATTATCTCTTGCATATTCGTAATAGTAATTGTAAAGAGTATACGATAACAGTATAG
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TOPOLOGY: 11r
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ADDRESSEE:
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: NEW YORK
RY: UNITED STATES OF AMERICA
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 Curtis, Morris & Safford
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29-MAR-1995
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                                                   FLAVIVIRUS RECOMBINANT POXVIRUS VACCINE
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                                                                                      Sequence 90, Application US/08484304; Patent No. 5744141; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US 0
FILING DATE: 17-7UL-1991
ATTORNEY/AGENT INFORMATION:
NAME: Frommer, William o
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REGISTRATION NUMBER: 25,506
REFERENCE/DOCKET NUMBER: 454310-2340
TELECOMMUNICATION INFORMATION:
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PRIOR APPLICATION DATA:
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APPLICANT: Pincus, Steven TITLE OF INVENTION: FLAVIV NUMBER OF SEQUENCES: 93 CORRESPONDENCE ADDRESS:
                                                       APPLICANT:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
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STREET: 530 Fifth Avenue
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                                                                            Paoletti, Enzo
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                      FLAVIVIRUS RECOMBINANT POXVIRUS VACCINE: 93
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ETLING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION UNBER: US/08/224,391
FILING DATE: 17-UI-1991
APPLICATION NUMBER: US 07/729,800
FILING DATE: 17-UI-1991
ATTORNEY/AGENT INFORMATION:
NAME: FTONMEC, William 5.
REGISTRATION NUMBER: 25,506
REFERENCE/DOCKET NUMBER: 454310-2340
TELECOMMUNICATION INFORMATION:
THE INFORMATION INFORMATION:
TELECOMMUNICATION INFORMATION:
Search completed: September 9, 2002, 02:46:17 Job time: 8114 sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 3209 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
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ADDRESSEE: C/O William S. Frommer
STREET: 530 Fifth Avenue
CITY: New York
STATE: New York
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